

GenData version 4.5
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CM Protein (protein search) using sw model

Run on: January 27 2000 09:55:41 Search time 46.01 seconds
(without alignments)
38,676 Million cell updates

Title: US-09-386-501-50

Perfect score: 136

Sequence: 1 IDP0110MFKSWKLVVHVSLS 26

Scoring table:

Scoring table: R0000062

Database:

SPTREX01_12.*

Word size: 0

Number of hits that pass the threshold: 225878

1: SP_archaea:
2: SP_bacteria:
3: SP_fungi:
4: SP_human:
5: SP_invertebrate:
6: SP_mammal:
7: SP_mold:
8: SP_ornithella:
9: SP_phage:
10: SP_plant:
11: SP_protist:
12: SP_virus:
13: SP_vertebrate:
14: SP_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is a rough estimate of the significance of the result.

SUMMARIES

Result	Query	%	Match	Length	Score	Identity
1	50	36.0	567	3	01210	012108 saccharomy
2	47	21.6	413	3	01791	017911 chondrichth
3	47	34.6	528	3	01792	017924 chondrichth
4	47	34.6	528	3	01792	017924 chondrichth
5	46.5	34.2	792	11	03519	03518 mus musculu
6	46	37.8	467	11	01765	017651 xenopus lae
7	45.5	38.5	982	4	024912	024912 homo sapien
8	45	38.5	982	4	024912	024912 homo sapien
9	45	38.1	814	4	01466	014666 homo sapien
10	45	38.1	814	4	01798	017988 homo sapien
11	45	38.1	814	4	01798	017988 homo sapien
12	45	38.1	598	5	01691	016911 homo sapien
13	45	38.1	598	5	01691	016911 homo sapien
14	45	38.1	598	5	01691	016911 homo sapien
15	44	32.4	938	5	061264	061264 caenorhabd
16	44	32.4	938	5	061264	061264 caenorhabd
17	43.5	32.0	430	11	008845	008845 ratius norv
18	43.5	32.0	430	11	008845	008845 ratius norv
19	43.5	32.0	430	11	008845	008845 ratius norv
20	43	31.6	246	1	068551	068551 pyrococcus
21	43	31.6	246	1	068551	068551 pyrococcus
22	43	31.6	246	1	068551	068551 pyrococcus
23	43	31.6	246	1	068551	068551 pyrococcus
24	43	31.6	246	1	068551	068551 pyrococcus
25	42	30.9	270	1	058587	058587 methanoco

26	42	30.9	138	1	06987	06987 aeropyrum p
27	42	30.9	138	1	06987	06987 aeropyrum p
28	42	30.9	138	1	06987	06987 aeropyrum p
29	42	30.9	138	1	06987	06987 aeropyrum p
30	42	30.9	138	1	06987	06987 aeropyrum p
31	42	30.9	138	1	06987	06987 aeropyrum p
32	42	30.9	138	1	06987	06987 aeropyrum p
33	42	30.9	138	1	06987	06987 aeropyrum p
34	42	30.9	138	1	06987	06987 aeropyrum p
35	42	30.9	138	1	06987	06987 aeropyrum p
36	42	30.9	138	1	06987	06987 aeropyrum p
37	42	30.9	138	1	06987	06987 aeropyrum p
38	42	30.9	138	1	06987	06987 aeropyrum p
39	42	30.9	138	1	06987	06987 aeropyrum p
40	42	30.9	138	1	06987	06987 aeropyrum p
41	42	30.9	138	1	06987	06987 aeropyrum p
42	42	30.9	138	1	06987	06987 aeropyrum p
43	42	30.9	138	1	06987	06987 aeropyrum p
44	42	30.9	138	1	06987	06987 aeropyrum p
45	42	30.9	138	1	06987	06987 aeropyrum p
46	42	30.9	138	1	06987	06987 aeropyrum p
47	42	30.9	138	1	06987	06987 aeropyrum p
48	42	30.9	138	1	06987	06987 aeropyrum p
49	42	30.9	138	1	06987	06987 aeropyrum p
50	42	30.9	138	1	06987	06987 aeropyrum p

ALIGNMENTS

RESULT 1

012108 PRELIMINARY: PRT: 567 AA.

012108 01-NOV-1996 (JEMBLrel_01, Created)

01-NOV-1996 (JEMBLrel_01, last sequence update)

01-NOV-1996 (JEMBLrel_01, last annotation update)

Y083263M FROM CHROMOSOME XV.

Y083263M OR 08263.

Saccharomyces cerevisiae (Strain's yeast).

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

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Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

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Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

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Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

Yeast, *Saccharomyces cerevisiae* Hemispheromyces; Saccharomyces.

[illegible]

RT : "Logans" :
RL : Nature 368:32-38(1994) :
RN : [3] :
SEQUENCE FROM N.A. :
FA : IDENTIFY :
6 : SUBMITTED (MAY-1995, TO THE LHM, GROUPED WITH 43143895, :
EMBL: Z73896; CAA98061.1 : JOINED. :
DK : EMBL: Z73422; CAA98061.1 : JOINED. :
DP : EMBL: Z73422; CAA97772.1 : JOINED. :
LR : EMBL: Z73896; CAA97772.1 : JOINED. :
SC : EMBL: 525 AA; 59493 MW; 46308904 CRC32 :
SEQUENCE :
Query Match : 34.6% : Score 47 : DB 5 : Length 525 :
Best Local Similarity : 38.1% : Prod. No. 19 :
Matches : 2 : Conservative : 1 : Mismatches : 6 : Gaps : 7 :
6 : LHMDFPKHLVDFLOSLS 26 :
11 : 11 : 11 : 11 : 11 :
D5 : 487 LLMHINPKTIVSDVPSIS 507 :
RESULT 4 :
624475 : PRELIMINARY : PRT : 628 AA :
19 : 624475 :
A5 : 024475 :
D1 : 01-JAN-1998 (ITEMBL:rel. 05, created) :
D1 : 01-JAN-1998 (ITEMBL:rel. 05, last sequence update) :
D1 : 01-NOV-1999 (ITEMBL:rel. 12, last annotation update) :
D1 : 01-NOV-1999 (ITEMBL:rel. 12, last annotation update) :
D1 : PINENE SYNTHASE. :
DN : AG3.18. :
GN : Abies grandis. :
OS : Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; :
OC : Eukaryota; Viridiplantae; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; :
OT : Abies. :
RN : [1] :
RN : SEQUENCE FROM N.A. :
RP : MEDLINE: 57415772. :
RX : "HIMMELMAN J. STEELE C.L. GROTEAU R. :
R6 : "Monoterpene synthases from grand fir (Abies grandis): cDNA isolation, :
RT : characterization, and functional expression of myrcene synthase." :
R1 : (45) -limonene synthase, and (-)-(1S,5S)-pinene synthase." :
R1 : J. Biol. Chem. 273:21784-21792(1997). :
R1 : EMBL: Z97969; AAB71085.1 :
DR : HSSP: Q40577; 5EAS. :
DR : MENDEL: 27004; Abisgf:2508;27004. :
DR : PFAM: PF01397; terpene_synth_1. :
SC : SEQUENCE : 628 AA; 71505 MW; ENCAPP51 CRC32 :
Query Match : 34.6% : Score 47 : DB 10 : Length 628 :
Best Local Similarity : 47.6% : Prod. No. 23 :
Matches : 11 : Conservative : 3 : Mismatches : 7 : Indels : 2 : Gaps : 1 :
6 : LHMDFPKHLVDFLOSLS 26 :
11 : 11 : 11 : 11 : 11 :
D5 : 490 LLMHINPKTIVSDVPSIS 512 :
RESULT 5 :
625218 : PRELIMINARY : PRT : 782 AA :
19 : 625218 :
AC : 035218 :
D1 : 01-JAN-1998 (ITEMBL:rel. 05, created) :
D1 : 01-JAN-1998 (ITEMBL:rel. 05, last sequence update) :
D1 : 01-JAN-1998 (ITEMBL:rel. 05, last annotation update) :
DE : CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR. :
GN : MCPSE. :
OS : Mus musculus (Mouse). :
OC : Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; :
OT : Eutheria; Rodentia; Sciurostomatia; Muridae; Murinae; Mus :
RN : [1] :
RN : SEQUENCE FROM N.A. :

THE MATRIX METALLOPROTEINASES IN
IN MN²⁺ MN²⁺
Homo sapiens (human) : Vertebrata : Mammalia
PUMILIONA : Mollusca : Turbellaria

DR 100045; hemopexin; 4.
 DR PFAM; PF00413; peptidase_M10; 1.
 DR PFAM; pf00134; MATRILIN.
 DR PRINTS; 598 AA; 65161 MW; 17360127 GPCR32

Page 4
 11 by 11

Query Match 33.1% Score 45. DB 5. Length 579
 Best Local Similarity 52.4% Prod No 44
 Matches 11 Conservative 2 Mismatches 8 Indels 0 Gaps 0

QY 6 LLOMDGFPKHLVDFLOS 26
 1 111 1111 1 1111
 DB 472 IFQMSGFYTFIRGLCFYS 492

RESULT 13

061264

ID 061264 PRELIMINARY ERI 579 AA.

AC 061264

DI 01-AUG-1998 (ITEMBLREL 07, Created)

DI 01-AUG-1998 (ITEMBLREL 07, Last sequence update)

DI 01-NOV-1999 (ITEMBLREL 12, Last annotation update)

DE MATRIX METALLOPROTEINASE

OS Caenorhabditis elegans

OC Eukaryota Metazoa Nematoda, Secernentea Eubelonia, Eubeloniidae

OC Phalloidina Phalloididae Phalloididae Polychaeta Cephalothorax Cephalothoracidae

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-N2

RA MADA K., SATO H., KINOSHITA K., KATITA Y., YAMAMOTO H., SETSU M.

RT Cloning of three Caenorhabditis elegans genes potentially encoding

RI novel matrix metalloproteinases.

FI Gene 211:57-62(1998)

DR EMBL: AB009916; FAA38951 1 -

DR HSSP: P03956; IAYK

DR HSSP: P03956; IAYK

DR PFAM: PF00413; peptidase_M10.1

DR PRINTS: PRO0138; MAIRIXIN

DR SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

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SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

SPANIN F 179 AA 1111 1111 1111 1111

Query Match 33.1% Score 44. DB 5. Length 579
 Best Local Similarity 52.4% Prod No 44
 Matches 11 Conservative 2 Mismatches 8 Indels 0 Gaps 0

QY 2 LLOMDGFPKHLVDFLOS 26
 1 111 1111 1 1111
 DB 552 GLLTMDGFPKHLVDFLOS 576

RESULT 15

008835

ID 008835 PRELIMINARY ERI 430 AA.

AC 008835

DI 01-JUL-1997 (ITEMBLREL 04, Created)

DI 01-JUL-1997 (ITEMBLREL 04, Last sequence update)

DI 01-NOV-1999 (ITEMBLREL 12, Last annotation update)

DE SINAPTOGEMIN II

OS Rattus norvegicus (Rat)

OC Eukaryota Metazoa Chordata, Vertebrata, Mammalia

OC Eutheria Rodentia Sciurognathi Muridae Murinae Rattus

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN

RA VON POSER G., HITCHENCO K., SHAO X., PIZO J., SHUPRO T.C.

RT J. Biol. Chem. 273:10000-10004 (1998)

FI EMBL: AF009402; AAB59344.1 1 -

DR HSSP: P21707; IAYN

DR PFAM: PF00160; Q21.2

DR PRINTS: PRO0138; SINAPTOGEMIN

DR SPANIN F 430 AA 1111 1111 1111 1111

SPANIN F 430 AA 1111 1111 1111 1111

SPANIN F 430 AA 1111 1111 1111 1111

SPANIN F 430 AA 1111 1111 1111 1111

SPANIN F 430 AA 1111 1111 1111 1111

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Thu Jan 27 11:30:51 2000

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